

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoehr/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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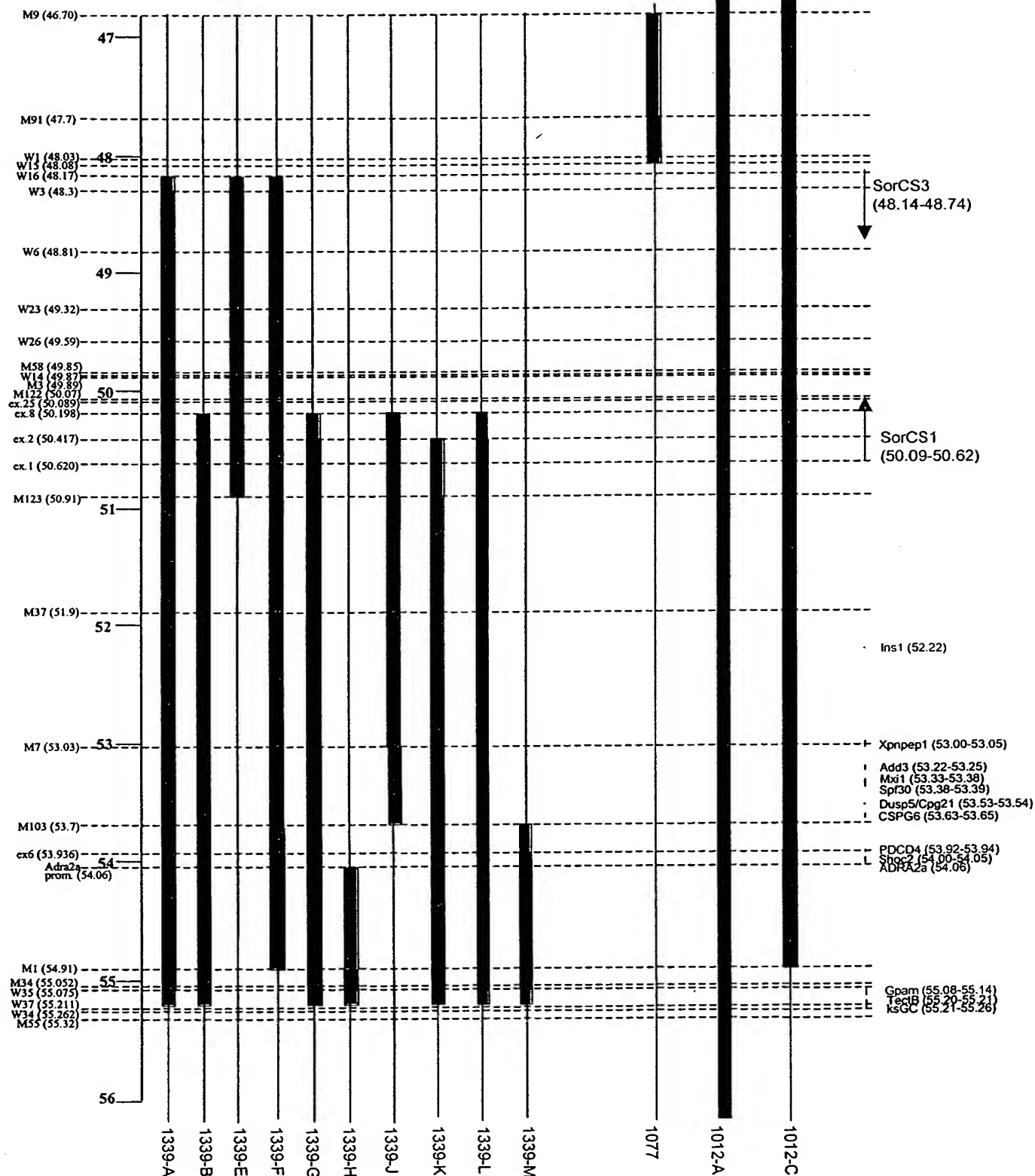


FIG 1

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES
Inventor(s): Attie/Stoehr/Schueler/Clee
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Sequence 1: mSorLA 2033 aa
Sequence 2: mSort 825 aa
Sequence 3: Vps10p 1577 aa
Sequence 4: mCS2 1159 aa
Sequence 5: hCS3 1223 aa
Sequence 6: mCS3 1219 aa
Sequence 7: mCS1a 1147 aa
Sequence 8: mCS1b 1167 aa
Sequence 9: mCS1c 1178 aa
Sequence 10: hCS1 1168 aa
Aligning...

Sequences (1:2) Aligned. Score: 20
Sequences (1:3) Aligned. Score: 8
Sequences (1:4) Aligned. Score: 18
Sequences (1:5) Aligned. Score: 16
Sequences (1:6) Aligned. Score: 15
Sequences (1:7) Aligned. Score: 13
Sequences (1:8) Aligned. Score: 14
Sequences (1:9) Aligned. Score: 13
Sequences (1:10) Aligned. Score: 14
Sequences (2:3) Aligned. Score: 16
Sequences (2:4) Aligned. Score: 20
Sequences (2:5) Aligned. Score: 20
Sequences (2:6) Aligned. Score: 20
Sequences (2:7) Aligned. Score: 21
Sequences (2:8) Aligned. Score: 21
Sequences (2:9) Aligned. Score: 20
Sequences (2:10) Aligned. Score: 21
Sequences (3:4) Aligned. Score: 11
Sequences (3:5) Aligned. Score: 11
Sequences (3:6) Aligned. Score: 11
Sequences (3:7) Aligned. Score: 10
Sequences (3:8) Aligned. Score: 11
Sequences (3:9) Aligned. Score: 10

Sequences (3:10) Aligned. Score: 10
Sequences (4:5) Aligned. Score: 42
Sequences (4:6) Aligned. Score: 42
Sequences (4:7) Aligned. Score: 42
Sequences (4:8) Aligned. Score: 42
Sequences (4:9) Aligned. Score: 43
Sequences (4:10) Aligned. Score: 42
Sequences (5:6) Aligned. Score: 92
Sequences (5:7) Aligned. Score: 63
Sequences (5:8) Aligned. Score: 62
Sequences (5:9) Aligned. Score: 64
Sequences (5:10) Aligned. Score: 63
Sequences (6:7) Aligned. Score: 63
Sequences (6:8) Aligned. Score: 62
Sequences (6:9) Aligned. Score: 63
Sequences (6:10) Aligned. Score: 61
Sequences (7:8) Aligned. Score: 98
Sequences (7:9) Aligned. Score: 97
Sequences (7:10) Aligned. Score: 91
Sequences (8:9) Aligned. Score: 96
Sequences (8:10) Aligned. Score: 93
Sequences (9:10) Aligned. Score: 90

CLUSTAL W (1.82) multiple sequence alignment

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mSorLA      YA QYLWITDFCST IHGFSIPFRAAD LLLHSKASNLLL GFDRSHPNKQLW KSDDFGQTWI 60
mSort      -----
Vps10p      -----MILLH 5

      :.      :.      :.      :.      :.      :.      :.      :.      :.      :.

mSorLA      MI QEHVKSFSWGID PYDQPNAIYIER HEPFGFSTVLRSTDFQSRNQEVILEEVRDFQL 120
mSort      -----
Vps10p      FV YSLWALLLIPLI NAEFTPKVTKT IAQDSFEILSFDDSNLIRKQDAS VTISFDDGET 65
      .. ..      .      .      .      .      .      .      .      .

mSorLA      RD KYMFATKVHLP GSQQQSSVQLWV SFGKPMRAAQFVTKHPINEYYIA DAAEDQVFCV 180
mSort      -----MERPRG AADG----- 10
Vps10p      WE KVEGIEDEITWI YIDPFNRHRAVATSMYESRLYITNDQGKSWERITLPDSEK---NI 122
mCS2      -----MA HRGPPSAPKRP GPTAPDRSFQA 24
hCS3      -N MEAARTERPAGR PGAPLVRTGLLLLSTWVLGAEIT WDATGGPGRPAPASRPALSP 59
mCS3      -- MEAAGTERPAGWPGAPLARTGLLLLSTWVLGAEIT WGATGGPGRLVS PASRPPVLP 58
mCS1a      MG KVGAGDGYAG- LSALLAGAGLLML-----LAPGVCSSLSCCPPQHPSSTPR----RT 50
mCS1b      MG KVGAGDGSSAG- LSALLAGAGLLML-----LAPGVCSSLSCCPPQHPSSTPR----RT 50
mCS1c      MG KVGAGDGSSAG- LSALLAGAGLLML-----LAPGVCSSLSCCPPQHPSSTPR----RT 50
hCS1      MG KVGAGGGSQAR- LSALLAGAGLLIL-----CAPGVCSSGSCCPSPHPSSAPR----SA 50
                                         T50->I

mSorLA      VSHSNNSTNLYISE AEGLKFSLSLEN VLYSPGGAGSD TLVRYFANEPPA DFHRVEGLQG 240
mSort      -----LLRWPLGLLLLLQLLPPAAV G---QDRLDAPPPAPPLLRWAGP ----- 51
Vps10p      SS RGCYIETHPLNK NYFLAKCNYCEK TEVDNEENSGDEEGAPVIFNITRCTDKVFASNDG 182
mCS2      LLPPCWPRSWPLLLLLLVLAACGAM GRSPQGRQGGPG VQITRLLPAGRT ----- 74
hCS3      LS PRAVASQWPEELASARRAAVLGRR AGPELLPQQGGG RGGEMQVEAGGTSPAGERRGRG 119
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FIG 2A

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

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mCS3      LLPRAAENRWPEELASARRAAAPRRRSRLLEPL SQASR---GEIR TEAAGMSPEGAR WVPG 115
mCS1a     LT PRGFPHPGPLGR APATPPPLFMR-----PLFAVAPG DRALFLERAGGS -----R 96
mCS1b     LT PRGFPHPGPLGR APATPPPLFMR-----PLFAVAPG DRALFLERAGGS -----R 96
mCS1c     LT PRGFPHPGPLGR APATPPPLFMR-----PLFAVAPG DRALFLERAGGS -----R 96
hCS1      ST PRGFHQGRPGR APATPLPLVVR-----PLFSVAPG DRALSLERARGT -----G 96

mSorLA    VY IATLINGSMNEE NMRSVITFDKGGTWEFLQAPAFITGYGEKINCELSQGCSSLHLAQRLS 300
mSort     -----VGVSWSGLR AAAPGGPVPRAG RWRRGAPAEQD CGRLP----- 88
Vps10p    GK SFSEIKSSLE-R NENSAISISDCG FAKTGKDSLESSDTSIIICLFQNM QLIMDEFSS- 240
mCS2      ---ESGDRKDPQAR ESEPSVPGGLPGSASGPSTDGAPAPGKRRARAVPVAGAASASR-- 129
hCS3      IPAPAKLGGARRSRRAQPPITQERGD AWATAPADGSR--GSRPLAKGSREEVKAPRAGG- 176
mCS3      IP SPSQAGSARRTRRAQPPSPLEGRD SWATALADGAK--GSRPHTKGSREEVRATRTGG- 172
mCS1a     VS VATAARSGRRRR SGTEPEKIEPGE GASRSRRDMLKD GGQQGLGTGARD PGKATRFR-- 154
mCS1b     VS VATAARSGRRRR SGTEPEKIEPGE GASRSRRDMLKD GGQQGLGTGARD PGKATRFR-- 154
mCS1c     VS VATAARSGRRRR SGTEPEKIEPGE GASRSRRDMLKD GGQQGLGTGARD PGKATRFR-- 154
hCS1      AS MAVAARSGRRRR SGADQEKAERGE GASRSPRGVLRD GGQQEPGTRERD PDKATRFR-- 154
          ^furin?      ^furin?      :

mSorLA    QLLNLQLRMPILS KESAPGLIIATGSVGKNLASKTNV YISSAGARWRE ALPGPHYITW 360
mSort     -----DFIA KLTNNTHQHVFDLSDSGSVSLSW 114
Vps10p    -----PYTES KLVLTDDWGKSL KEFDQFKDKV 267
mCS2      -----AQV SLISTSFVLKGDATHNQAMVHW 154
hCS3      -----SAAEDL RLPSTSFALTGD SAHNQAMVHW 204
mCS3      -----ASTEEL RLPSTSFALTGD SAHNQAMVHW 200
mCS1a     -----MEEL RLTSTTFALTGD SAHNQAMVHW 180
mCS1b     -----MEEL RLTSTTFALTGD SAHNQAMVHW 180
mCS1c     -----MEEL RLTSTTFALTGD SAHNQAMVHW 180
hCS1      -----MEEL RLTSTTFALTGD SAHNQAMVHW 180
          . . . . . : . . . . . : . . . . . : . . . . .

mSorLA    GD HGGIIMAIQGM ETNELKYSTNEG ETWKTFFVSEKPVFVYGLLTPEPGE KSTVFTIFGS 420
mSort     VG DSTGVILVLTTF QVPLVIVSFGQS KLYRSEDYGNK----FKDITNLINNTFIRTEFGM 170
Vps10p    VNGYRILKSHMVVI TQGDYNDMSSM DVVWSNDLSNFR MAYMPTQLRHSM QGEIYEDAMG 327
mCS2      TG ENSSVILILTKYYH-ADMGKVLESSLWRSSDFGTT----YTKLTLQPG VTTVIDNF-- 207
hCS3      SGHNSSVILILTKL YD-FNLGSVTESSLWRSTDYGT----YEKLNKVG LKTVLSYL-- 257
mCS3      SGHNSSVILILTKL YD-FNLGSVTESSLWRSTDYGT----YEKLNKVG LKTVLSYL-- 253
mCS1a     SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT----YEKLNKVG LKTVLSYL-- 233
mCS1b     SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT----YEKLNKVG LKTVLSYL-- 233
mCS1c     SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT----YEKLNKVG LKTVLSYL-- 233
hCS1      SGHNSSVILILTKL YD-YNLGSITESSLWRSTDYGT----YEKLNKVG LKTVLSYL-- 233
          . . . . . : . . . . . : . . . . . : . . . . .

mSorLA    NK ESVHSLILQVN ATDALGVPCTEN DYKLWSPSDEGNECLLGHKTVFKRRTPHATCFN 480
mSort     -----AIGPENSGKVILTAEVSG ----- 188
Vps10p    -----RIILPMS RERSDQEED----- 343
mCS2      -----YICPAN KRKIIIVSSSL----- 224
hCS3      -----YVNPTN KRKIMLLSD----- 272
mCS3      -----YVNPTN KRKIMLLSD----- 268
mCS1a     -----YVCPTN KCKIMLLTD----- 248
mCS1b     -----YVCPTN KCKIMLLTD----- 248
mCS1c     -----YVCPTN KCKIMLLTD----- 248
hCS1      -----YVCPTN KRKIMLLTD----- 248
          . . . . . : . . . . . : . . . . . : . . . . .

mSorLA    GEDFDRPVVVSNCSTREDYECDFGF KMSEDLSLEVCPDPEFFGKPYSPVPVPCVGVSSY 540
mSort     GS RGRVFRSSDFA KNFVQTDLPFHP -----LTQMYS PQNSDYLLALST ENGLWVSKNF 243
Vps10p    KG IVSEILISDSQG LKFSPIPWANE VFG-YINLYQPTYLKGTMIASLYPLSRRNRKRGK 402
mCS2      GD REQSLFLSTDEG ATFQKYPVPFL-----VETLLFH PKEEDKVLAYTK DSKLYVSSDL 278

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FIG 2B

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

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hCS3      PEMESSILISSDEGATYQKY RLTFY-----IQSLLFHPKQEDWVLAYS LDQKLYSSMDF 326
mCS3      PE MESSVLISSDEG ATYQKYRLTFY-----IQSLLFH PKQEDWVLAYS LDQKLYSSMDF 322
mCS1a     PE IESSLLISSDEG ATYQKYRLNFI-----LQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
mCS1b     PE IESSLLISSDEG ATYQKYRLNFI-----LQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
mCS1c     PE IESSLLISSDEG ATYQKYRLNFI-----LQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
hCS1      PE IESSLLISSDEG ATYQKYRLNFI-----IQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
. . . . .

mSorLA    RR TRGYRKISGDTCSGGDVEARLEGE LVPCPLAEENEFILYAMRKFIYRY DLASGATEQL 600
mSort     G--EKWEEIHK-----AVCLAK WGPNNIIFFTTH VNGSCKADLGAL ELWRTSDLGK 292
Vps10p    AK GVKNGKGVTKISV DNGLTWTVLKVV DPNADSFDCDI TDFENC SLQNM F YTREGSTPTA 462
mCS2      G--KKWTLQERV T KDHVFWAVSGVDDDPNLVHVEAQD LSGGYRYTTC LI YNCSAQPHIA 336
hCS3      G--RRWQLMHERIT PNRFYWSVAGLD KEADLVHMEVRTTDGYAHYLTCRI QECAETTRSG 384
mCS3      G--RRWQLMHERIT PNRFYWSVAGLD KEADLVHMEVRT ADGYAHYLTCRI QECAETTRSG 380
mCS1a     G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGH SIYLT CRM QNCTEANRNK 360
mCS1b     G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGH SIYLT CRM QNCTEANRNK 360
mCS1c     G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGH SIYLT CRM QNCTEANRNK 360
hCS1      G--RRWQLIQEGVVPNRFYWSVMGSN KEPDLVHLEART VDGH SHYLT CRM QNCTEANRNQ 360
. . . . .

mSorLA    PL SGLRAAVALDFGYERNCLYWSDLALDTIQRLCLNGSTGQEV I INSGLE TVEALAFEPL 660
mSort     TF KTIG-----VKIYSFG LGGRFLFASE 315
Vps10p    GILMTTG-----IV GDGSVFDWGDQR TPI SRDGGLTWK LAFDFPCLYAVG DYGNVIVAIP 517
mCS2      PF SGP-----IDRGS LT VQDEYIFLKA 358
hCS3      PFARS-----IDISSLVVQDEYIFIQV 406
mCS3      PFARS-----IDISSLVVQDEYIFIQV 402
mCS1a     PFPGY-----IDPDSLIVQDDYVVFVQL 382
mCS1b     PFPGY-----IDPDSLIVQDDYVVFVQL 382
mCS1c     PFPGY-----IDPDSLIVQDDYVVFVQL 382
hCS1      PFPGY-----IDPDSLIVQDHYVVFVQL 382
. . . . .

mSorLA    SQ LLYWVDAGFKKI EVANPDGDFRLT IVNSSVLD RPRALVLPQEGVMFW TDWGD LKPGI 720
mSort     MA DK---DTTRRIH VSTDQGD TWSMA QLP SVGQE QFYS ILAANEDMVFMH VDE----- 365
Vps10p    YN ADEDDDPQSEFYYS LDQGKTWTEYQLETTIYPNEVM NTPD GSGAKFILNG-----F 571
mCS2      TS -----TNRTKYVSYRRSDFVLM KLPKYALPKDLQ IISTDEQQVFVAVQE----- 405
hCS3      TT -----SGRASYYVS YRREAF AQI KLPKYS LPKDMH IISTDENQVF AAVQE----- 453
mCS3      TI -----GGRASYYVS YRREAF AQI KLPKYS LPKDMH IISTDENQVF AAVQE----- 449
mCS1a     TS -----GGRPHYVVS YRRSPFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
mCS1b     TS -----GGRPHYVVS YRRSPFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
mCS1c     TS -----GGRPHYVVS YRRSPFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
hCS1      TS -----GGRPHYVVS YRRNAFAQM KLPKYALPKDMH VISTDENQVF AAVQE----- 429
. . . . .

mSorLA    YR SYMDGSAAYRLV SEDVKWPNGISV DS-----QWIYWT DAYLDC IERITFSGQQ 770
mSort     ---PGDTGFGTIFTSDDRGI VYSKSL DR-----HLYTTTG---ETDFTNVTSLR 409
Vps10p    TLAHMDGTTNFIY AIDFSTAFNDKTC EENDFEDWNLAEGKCVNGVKYKIRRRKQDAQCLV 631
mCS2      ---WNQVD TYNLYQSDLRGVRYSLVL EN-----VRSSRQAENNV IDILEVRGVK 452
hCS3      ---WNQND TYNLYI SDTRGIYFTLAM EN-----IKSSRGLMGNII IELYEVAGIK 500
mCS3      ---WNQND TYNLYI SDTRGIYFTLAM EN-----IKSSRGLMGNII IELYEVAGIK 496
mCS1a     ---WNQND TYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNV MIDLYEVAGIK 476
mCS1b     ---WNQND TYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNV MIDLYEVAGIK 476
mCS1c     ---WNQND TYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNV MIDLYEVAGIK 476
hCS1      ---WNQND TYNLYI SDTRGVYFTLAL EN-----VQSSRGPEGNIMIDLYEVAGIK 476

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FIG 2C

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::      :      :
mSorLA      RSVILDSLPHPYAIAVFKNEIYWDDWSQLSIFRAS KHSRSQVEILASQLTGLMDMKVFY K 830
mSort      GV YITSTLSEDNSI QSMITFDQGGRW EHLRKP-ENSKC DA----- 448
Vps10p      KK VFEDLQLFETAC DKCTEADYECAF EFVRDATGKCV DYN-----L 673
mCS2      GVFLAN-QKVDGKV TTVITYNKGRDW DYLRPPSTDMNG KP----- 491
hCS3      GIFLAN-KKVDDQV KTYITYNKGRDW RLLQAPDVLGRSP----- 539
mCS3      GIFLAN-KKVDDQV KTYITYNKGRDW RLLQAPDVLGRSP----- 535
mCS1a      GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP----- 515
mCS1b      GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP----- 515
mCS1c      GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP----- 515
hCS1      GMFLAN-KKIDNQV KTFITYNKGRDW RLLQAPDADLRG DP----- 515
          : .          : :          . .      : : . . .

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```

mSorLA      GK NAGSNACVPQPCSLCLPKANNSK SCRCPEGVASSVLP SGDL MCD CPQGYQRKNNTCV 890
mSort      -----TAKNKNECSLHIHASYSISQ KLNVPMAPLSEP NAVGIVIAHG----- 490
Vps10p      IVLSDVCDKTKKKT VPKPLQLVKGD KCKKPMTVKSVD ISCEGVPKKG----- 721
mCS2      -----TNCQPPDCYLHLHLRWADNP YVSGTVH--TKD TAPGLIMGAG----- 531
hCS3      -----VHCLLPFCSLHLHLQLENP YSSGRIS--SKE TAPGLVVATG----- 579
mCS3      -----VHCLLPFCSLHLHLQLENP YSSGRIS--SKD TAPGLVVATG----- 575
mCS1a      -----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SRD TAPSIIVASG----- 555
mCS1b      -----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SRD TAPSIIVASG----- 555
mCS1c      -----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SRD TAPSIIVASG----- 555
hCS1      -----VHCLLPYCSLHLHLKVS ENP YTSGIIA--SKD TAPSIIVASG----- 555
          : .          : .      : . . . . .

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mSorLA      KEENTCLRNQYRCSNGNCINSIWWD FDND CGDMSDER NCPTTVCDADTQ FRCQESGTCI 950
mSort      -----
Vps10p      -----
mCS2      -----
hCS3      -----
mCS3      -----
mCS1a      -----
mCS1b      -----
mCS1c      -----
hCS1      -----
          : . . . . . : . . . . . : . . . . . : . . . . .

```

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mSorLA      PL SYKCDLEDDCGD NSDESHCEMHQC RSDEFNCSSGMC IRSSWVCDGDND CRDWSDEANC 1010
mSort      -----SVGD AISVMVPDVYIS D-----DGGYS WAKMLEGPHY 522
Vps10p      -----TNDK EIVVTENKFDK IQFYQYFDTVTDESLLMINSRGEA YISHDGGQTI 771
mCS2      -----NLGSQLVEYKEEMYITS-----DCGHT WRQVFEEHH 563
hCS3      -----NIGP ELSYTDIGVFISS-----DGGNT WRQIFDEEYN 611
mCS3      -----NIGS ELSYTDIGVFISS-----DGGNT WRQIFDEEYN 607
mCS1a      -----NIGS ELSDSDISMVSS-----DAGNT WRQIFEEHHS 587
mCS1b      -----NIGS ELSDSDISMVSS-----DAGNT WRQIFEEHHS 587
mCS1c      -----NIGS ELSDSDISMVSS-----DAGNT WRQIFEEHHS 587
hCS1      -----NIGS ELSDTDISMVSS-----DAGNT WRQIFEEHHS 587
          : . . . . . : . . . . . : . . . . . : . . . . .

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mSorLA      TAIYHTCEASNFOCHNGHCIPQRWAC DGDADCQDGSDEDPVSCEKKCNF HCPNGTCIPS 1070
mSort      YT ILDSGGIIIVAE HSNRPINVIKFSTDEGQC-----WQSVFTQE 563
Vps10p      RR FDSNGETIIEVFNPPYNNSSAYLF GSKGSIFS-----THDRGYSFMTA 816
mCS2      VL YLDHGGVIAAIK DTSIPLKILKFS VDEGHT-----WSTHNFTST 604

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FIG 2D

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hCS3	VWFLDWGGALVAMKHTPLPVRH LWVSFDEGHS-----WDKYGFTSV 652
mCS3	VWFLDWGGALVAMK HTPLPVRHLWVS FDEGHS-----WDKYGFTLL 648
mCS1a	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
mCS1b	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
mCS1c	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
hCS1	VL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628

mSorLA	SK HCDGLRDCPDGS DEQHCEPFCTRFMDVFCNRRQQCLFHSMVCDGIVQC RDGSDEDAAF 1130
mSort	PI YFTGLASEPGA----- 576
Vps10p	KLPEARQLGMPLDF N----- 831
mCS2	SVFVDGLLSEPGD----- 617
hCS3	PLFVDGALVEAGM----- 665
mCS3	PLFVDGALVEAGV----- 661
mCS1a	PLFVDGVLGEPGE----- 641
mCS1b	PLFVDGVLGEPGE----- 641
mCS1c	PLFVDGVLGEPGE----- 641
hCS1	PLFVDGVLGEPGE----- 641

mSorLA	AGCSQDPEFHKECDEFGFCQNGVCI SLIWKCDGMDDCGDYSDEANCENP TEAPNCSRYF 1190
mSort	-----RSMNISIW GFTESFITRQWV SYTVDFKDIL 606
Vps10p	-----AKAQDTFIYYGGRNCESILSPECHAVAYLTNDGGE TFTEMLDNAI 876
mCS2	-----ETLVMTVF GHIS--FRSDWE LVKVDFRPSF 645
hCS3	-----ETHIMTVF GHFS--LRSEWQ LVKVVDYKSIF 693
mCS3	-----ETHIMTVF GHFS--LRSEWQ LVKVVDYKSIF 689
mCS1a	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
mCS1b	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
mCS1c	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
hCS1	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669

mSorLA	QF HCENGHCIPNRW KCDRENDGCDWS DEKDCGDSHVLP SPTPGPSTCLPNYFRCSGACV 1250
mSort	ER NCE-----EDDYTTWLAHSTD-----PGDYKDGC I 633
Vps10p	HC EFAGSLFKYPSN EDMVMCQVKEKSSQTRSLVSSTDFQDDKNTVFENIIGYLSTGGYI 936
mCS2	PR QCG-----EDDYSSWD LTDL-----QGDDHCI 668
hCS3	SR HCT-----KEDYQTHW LLN-----QGEPCV 715
mCS3	SRRCT-----KEDFETWH LLN-----QGEPCV 711
mCS1a	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
mCS1b	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
mCS1c	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
hCS1	DRRCA-----EEDYRPWQ LHS-----QGEACI 691

mSorLA	MGTWVCDGYRDCAD GSDEEACPSLANSTAAPTQLGQCDFEFECHQPKKCI PNWKRC D 1310
mSort	LG -----YKEQFLRLR 644
Vps10p	IVAVPHE-----NNELRAYVTID 954
mCS2	MG -----QORSYRKRK 679
hCS3	MG -----ERKIFKKRK 726
mCS3	MG -----ERKIFKKRK 722
mCS1a	MG -----AKRIYKKRK 702
mCS1b	MG -----AKRIYKKRK 702
mCS1c	MG -----AKRIYKKRK 702
hCS1	MG -----AKRIYKKRK 702

FIG 2E

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mSorLA      GHQDCQDQDE ANCPHTSTLTCTSTREFKCEDGEAC IVLSERCDGFLD CSDESDEKACSDE 1370
mSort      KSSVCQNGRDYVVA KQPSVCPCSLLED FLCDFGYFRPENAS-----ECVE QPELKGHELE 698
Vps10p     GT EFAEAKFPYDED VGKQEAFTILES EKGSIFLHLATN LVPGRDFGNLLK SNSNGTSFVT 1014
mCS2       STSWCVKGRSFTSALTSRVCKCRSD FLCDYGFERSSSSESTA--NKCSA NFWFNPLSPP 737
hCS3       PG AQCALGRDHSGS VVSEPCVCANWD FECDYGYERHGE SQ-----CVPAFWYNPASPS 779
mCS3       PG AQCALGREYSGS VVSEPCVCADWD FECDYGYERHGE SQ-----CVPAFWYNPASPS 775
mCS1a      SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 753
mCS1b      SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 753
mCS1c      SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 753
hCS1       SE RKCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSLS 754

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mSorLA      LT VYKVQNLQWTAD FSGDVTLTWMPR KKMPASACVYNV YYRVVGESIWK LETHSNTKTST 1430
mSort      FC LYGKEEHLTTNGYR-----KIPGDKCQGGM N-----PAREVK----- 732
Vps10p     LE HAVNRNTFGYVD FEKIQGLEGIIL TNIVSNSDKVAEN NKEDKQLKTKIT FNEGSDWN-- 1072
mCS2       ED CVLGQTYTSSLGYR-----KVVSNNCTDGL DLQSPVQLQCPLQAPR----- 781
hCS3       KD CSLGQSYLNSTGYR-----RIVSNNCTDGL REKYTAKAQMCPC GKAPR----- 823
mCS3       KD CSLGQSYLNSTGYR-----RIVSNNCTDGL RDKYSAKTQLCP GKAPR----- 819
mCS1a      KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 797
mCS1b      KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 797
mCS1c      KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 797
hCS1       KD CSLGQSYLNSTGYR-----KVVSNNCTDGV REQYTAKPQKCP GKAPR----- 798

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mSorLA      VL KVLKPDTTYQVK VQVHCLNKVHNTNDFVTLRTPEGLPDAPRNLQLSLN REEEGVILGH 1490
mSort      -----DLKKKCTSNFL NPTKQN----- 749
Vps10p     -----FLKPPKRDS EGKKFFCSSL DECSLHLHGYTE RKDIRDTYSS 1115
mCS2       -----GLQVSIERGEAVVRPREDVLFVV ROEQGDVLT 814
hCS3       -----GLHVVTTDGRLVAEQGHNATFIILMEEGDLQRT 856
mCS3       -----GLHVVTTDGRLVAEQGHNATFIILMEEGDLQRT 852
mCS1a      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
mCS1b      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
mCS1c      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
hCS1       -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 831

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```

mSorLA      WAPPVHTHGLIREY IVEYSRSGSKMWASQRAASNSTEI KNLLLNALYTVR VAAVTSRGIG 1550
mSort      -----SKNSVPIILAIVGLMLVTVVAG----- 772
Vps10p     GS ALGMMFGVGNVG PNLLPYKECSTFTTDDGETWAEV KKTPhQWEYGDHGILVLPEN 1175
mCS2       KYQVDLGDGFKAMY VNLTLTGEPRIHHYESPGIYRVSV RAENMAGHDEAVLFVQVNSPLQ 874
hCS3       NI QLDFGDGIAVSY ANFSPIEDGIKH VYKSAGI FQVTA YAENNLGSDTAVLFHLHVCPVE 916
mCS3       NI QLDFGDGIAVSY ANFSPIEDGIKH VYKSAGI FQVTA YAENNLGSDTAVLFHLHVCPVE 912
mCS1a      LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGI FRVTV QVDNSLGSDSAVLYLHVTCPLE 890
mCS1b      LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGI FRVTV QVDNSLGSDSAVLYLHVTCPLE 890
mCS1c      LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGI FRVTV QVDNSLGSDSAVLYLHVTCPLE 890
hCS1       LI QVDFGDGIAVSY VNLSSMEDGIKH VYQNVGI FRVTV QVDNSLGSDSAVLYLHVTCPLE 891

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mSorLA      NW SDSKSITTIKGV IAPNIHIDSY DENSLSFTLTMD GDIKVNGYVNLWFSFDAHKQE 1610
mSort      -----VLIVKKYVCGGR- 784
Vps10p     SE TDSISYSTDFGK TWKDYKFCADKVLVKDITTVPRDS ALRFLLFGEAAD IGGSSFRITYT 1235
mCS2       AL YLEVVPVIGVNQ EVNLTAVLLPLN PNLTVFYWWIGHSLQPLLSLDNSV TTKFTDAGDV 934

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FIG 2F

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoeck/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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hCS3	HVHLRVPFVAIRNKEVNISAVVWPSQLGTLTYFWWFGNSTKPLITL DSSISFTFLAEGTD 976
mCS3	HV HLRVPFVAIRNK DVNISAVVWPSQ LGTLTYFWWFGNSTKPLITLDSSI SFTFLAEGTN 972
mCS1a	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFKFTSEGMN 950
mCS1b	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFKFTSEGMN 950
mCS1c	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFKFTSEGMN 950
hCS1	HV HLSLPFVTTKNK EVNATAVLWPSQ VGTLYVWWYGNNTPLITLEGSI SFRFTSEGMN 951
.	
mSorLA	KK TLSFRGGSALSH KVSNLTAHTSYE ISAWAKTDLGDS PLAFEHILTRGSSPPAPSLKAK 1670
mSort	----FLVHRYSVLQQHAEADGVEALD STSHAKSGYHDD ----- 818
Vps10p	ID FRNIFERQCDFD ITGKESADYKYS PLSSKSNCLFGHQT----- 1275
mCS2	RV TVQAAACGNSVLQ DSRLVRLDQFQ VVPLRFSRELDT ----- 972
hCS3	TI TVQVAAGNALIQ DTKEIAVHEYFQSLLSFSPNLDY ----- 1014
mCS3	TI TVQVAAGNALIQ DTKEIAVHEYFQSLLSFSPNLDY ----- 1010
mCS1a	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLAFSPNLDD ----- 988
mCS1b	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLAFSPNLDD ----- 988
mCS1c	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLAFSPNLDD ----- 988
hCS1	TI TVQVSAGNAILQ DTKTIAVYEEFR SLRLSFSPNLDD ----- 989
. : . : : . : . : . : .	
mSorLA	AI NQTAVECIWTGP KNVVYGIFYATS FLDLYRNPKSVTTSLHNKTIVIVSK DEQYLFLVRV 1730
mSort	-----SDEDLLE----- 825
Vps10p	-----EFLRKTDENC FIGNIPLSEF 1295
mCS2	-----FNPNTPEWR EDVGLVVTRL 991
hCS3	-----HNPDIPEWRKDIGNVIKRA 1033
mCS3	-----HNPDIPEWR QDIGNVIKRA 1029
mCS1a	-----YNPDIPEWRDISRVIKKS 1007
mCS1b	-----YNPDIPEWRDISRVIKKS 1007
mCS1c	-----YNPDIPEWRDISRVIKKS 1007
hCS1	-----YNPDIPEWRDIGRVIKKS 1008
: . . . : . : . : . : . : . : .	
mSorLA	LIPYQGPSSDYVVV KMIPDSRLPPRH LHAVHIGKTSALIKWESPYDSPDQ DLFYAIAVKD 1790
mSort	-----
Vps10p	SR NIKNCSCTRQDF ECDYNFYKANDGTCKLVKGLSPAN AADVCKKEPDLI EYFESSGYRK 1355
mCS2	LS KETSIPEELLVT VVKPGLPTIADL YVLLPLPRPTRKRSLS--DKRLAAVQQALNSHR 1049
hCS3	LV KVTSPEDQILIAVFPGLPTS AELFILPPKNLTERRKGNEGDLEQIVE TLFNALNQNL 1093
mCS3	LI KVTSPEDQILVAVFPGLPTS AELFILPPKNLTERRKGHEGDLEQIVE TLFNALNQNL 1089
mCS1a	LV EATGIPSQHILVAVLPGLPTAAELFVLPYQDGTREN KRSPEDLEQISE VLIHKLNQNL 1067
mCS1b	LV EATGIPSQHILVAVLPGLPTAAELFVLPYQDGTREN KRSPEDLEQISE VLIHKLNQNL 1067
mCS1c	LV EATGIPSQHILVAVLPGLPTAAELFVLPYQDGTREN KRSPEDLEQISE VLIHKLNQNL 1067
hCS1	LV EATGVPQHILVAVLPGLPTAELFVLPYQDPAGEN KRSTDDLEQISE LLIHTLNQNS 1068
.	
mSorLA	LI RKTDRSYKVRSR NSTVEYSLSKLE PGGKYHIIIVQLGNMSKDSSIKITT VLSAPDALK 1850
mSort	-----
Vps10p	IPLSTCEGGLKLDAPSSPHACPGK-----EKE FKEYSVSAGPFAFIFISILLI 1404
mCS2	IS FILRGGLRILVE LRDTDTGP-----QRPGSGG-Y WAVVVLVFIG 1090
hCS3	VQ FELKPGVQVIVY VTQLTLAP-----LVDSSAGHSSSAMLMLLSVV 1135
mCS3	VQ FELKPGVQVIVY VTQLTLAP-----LVDSSAGHSSSAMLMLLSVV 1131
mCS1a	VH FELKPGVQVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1109
mCS1b	VH FELKPGVQVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1109
mCS1c	VH FELKPGVQVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1109
hCS1	VH FELKPGVRVLVH AAHLTAAP-----LVDLTPTHSGSAMLMLLSVV 1110

FIG 2G

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoeck/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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. . . . . ^ trans-

mSorLA      II TENDHVLLFWKS LALKEKQFNETR GYEIHMSDSAVN LTAYLGNTTDFNFFKVSNLKMGH 1910
mSort      -----
Vps10p      IFFAAWFVYDRGIRRNNGGFARFGEIR LGDDGLIENNNT DRVVNNIVKSGFYVFSNIGSLL 1464
mCS2        LFAVGAFILYKFKRKRPGRTVYAQMHNKEQEMTSPVSHSEDAQSTMQGNHSGVLSINS 1150
hCS3        FV GLAVFLIYKFKRKIPWINIYAQVQHDKEQEMIGSVSQSENAPKITLSD FT-EPEELLD 1194
mCS3        FV GLAVFLIYKFKRKIPWINIYAQVQHDKEQEMIGSVSQSENAPKITLSD FT-EPEELLD 1190
mCS1a       FV GLAVFVIYKFKR -----CVFLLP -----SYPRPPPPSSF CQ-VQKQ--- 1147
mCS1b       FV GLAVFVIYKFKRR----VALPSPP SPSAQPGDSSLR LQRPRPATPPSS PK-RGSAGAQ 1164
mCS1c       FV GLAVFVIYKFKRKIPGINVYAQMONEKEQELINPVSHSESRPSVPHPD LR-RPGQLVD 1168
hCS1        FV GLAVFVIYKFKRR----VALPSPP SPSTQPGDSSLR LQRARHATPPST PK-RGSAGAQ 1165
            -membrane^ .S1149->P

mSorLA      NYTFTVQARCLFGSQICGEPVLLYDELSSGADA AVIQ AARSTDVA AVVPILFLILLSL 1970
mSort      -----
Vps10p      QHTKTNI AHVISKI RGRFGNRTGPSYSSLIHDQFLDEA DDL LAGHDEDAN --DLSSFMDQ 1522
mCS2        RE MHSYLVG----- 1159
hCS3        KE LDTRVIGGIATIANSESTKEIPNCTSV----- 1223
mCS3        KE LDTRVIGSIATIASSESTKEIPNCTSV----- 1219
mCS1a       -----
mCS1b       FAI----- 1167
mCS1c       EK VESQLLGK----- 1178
hCS1        YAI----- 1168

: . . . .

mSorLA      GV GFAILYTKHRR LQSSFSAFANSHYSSRLGSAIFSSG DDLGEDDEDAPMITGFSDDVPM 2030
Vps10p      GSNFEIEEDDVPTL EEEHTSYTDQPTTDDVPDALPEGN EENIDRPDSTAP SNENQ----- 1577
. . . . . : : : : : : : : : : : : : : :

mSorLA      VIA 2033

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FIG 2H